
A walkthrough of the ratervar package

Zachary Stansell¹, Deniz Akdemir, Thomas Björkman

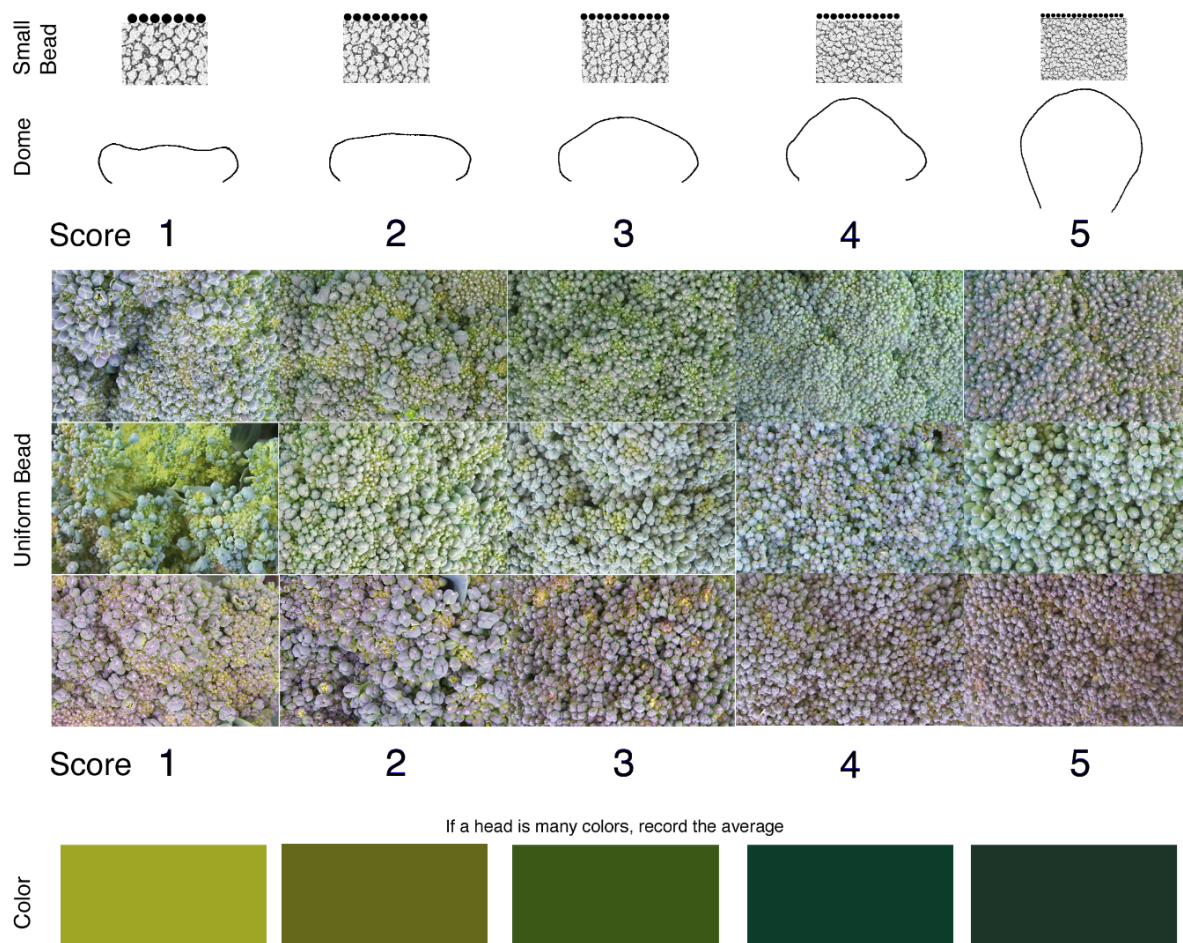
Section Horticulture, Cornell AgriTech
Cornell University– Geneva

[Björkman Lab](#)

January 23, 2019

About

During the course of the [Eastern Broccoli Project](#), we realized a need for flexible tools that would allow us to evaluate many different broccoli hybrids for many different traits within many distinct growth environments. Broccoli is a crop where not only yield but horticultural quality is important, so we were interested in understanding both the components that comprise high-quality broccoli and how such a perception might vary across individuals.



Broccoli Evaluation Scale. Eastern Broccoli Project 2011. Contact: T. Björkman, Cornell University info@cornell.edu
Developed by M. Farnham, T. Björkman, D. Couillard, J.W. Shail, Z. Stansell, W. Morris, A. Hamilton, J. Davis, J.P. Smith, M. Hutton, P.D. Griffiths

Scoring rubric for traits collected in Eastern Broccoli Project

¹ feel free to email any thoughts or questions to zjs29@cornell.edu

Objectives

Some of the key questions we wanted to address were:

1. How do we choose the best broccoli hybrid for a given growth environment?
2. How do we quantify the degree of head quality?
3. How many different traits do we need to efficiently capture variation in head quality?
4. To what extent do subjective human raters agree/disagree on head quality?
5. Can we define a “Quality Trait Index” that would allow us to both compare broccoli hybrids across many environments and be more robust to subjective human preferences?

Tools and lessons learned from this project are presented here as a R package `ratervar`. This document will provide a work though using a dataset generated from the Eastern Broccoli Project.

Publication: [Quality Trait Index to Increase the Reliability of Phenotypic Evaluations in Broccoli](#)

Preliminaries:

1. To install `ratervar`, download the `ratervar.tar.gz` ... and type (within R)

```
install.packages("/path_to_file/ratervar.X.X.tar.gz", repos=NULL, type="source")
```

where 'path_to_file' is the file path to where you've saved `ratervar.X.X.tar.gz`.

On Windows it will look something like this:

```
"C:\\\\DIR\\ratervar.X.X.tar.gz".
```

On UNIX it will look like this:

```
"/home/something/ratervar.X.X.tar.gz"
```

This needs to be done just once.

2. To load the `ratervar` package, type

```
library(ratervar)
```

This needs to be done every time you start R. `ratervar` depends on several other packages, R *should* automatically install them.

3. The best way to get help on the functions and data sets in R (and in **ratervar**) is via the html version of the help files.

```
help.start()
```

This should open a browser with the main help menu.

An alternative method to view this help file is to type one of the following:

```
help(ratervar)
?ratervar
```

or for a particular function:

```
help(qualityindex)
?qualityindex()
```

Relative Importance Analysis

1. To load the example dataset into R, type:

```
data(rv)
```

2. To see the columns of the dataset (Table 1), type:

```
head(rv)
```

Table 1: Column names of Eastern Broccoli Project dataset **rv**

Column	Description	Data Type
Uniq	Unique identifier for a given row. Not required.	character
Year	Trial year (1 or 2). Not required.	character
Planting	Specific planting within year (1 or 2). Not required	character
Env	Unique ID for environment (Year+Planting). Not required	character
Plot	Plot number. Not required.	character
Rater	Human rater who evaluated a given plot. Not required.	character
LineU	Unique Line (genotype) designation. Not required.	character
Rep	Replication (1,2,3,4). Not required.	character
OQ	Overall Quality Score	1-5
HE	Head Extension	1-5
PU	Plot Uniformity	1-5
HC	Head Color	1-5
HS	Head Shape	1-5
US	Head Uniformity/smoothness	1-5
HF	Head Firmness	1-5
BS	Bead Size	1-5
BU	Bead Uniformity	1-5
HA	Holding ability (how quickly does it bolt?)	1-5

3. To conduct relative importance analysis² on all of the data, using OQ (overall quality) as the response variable, run:

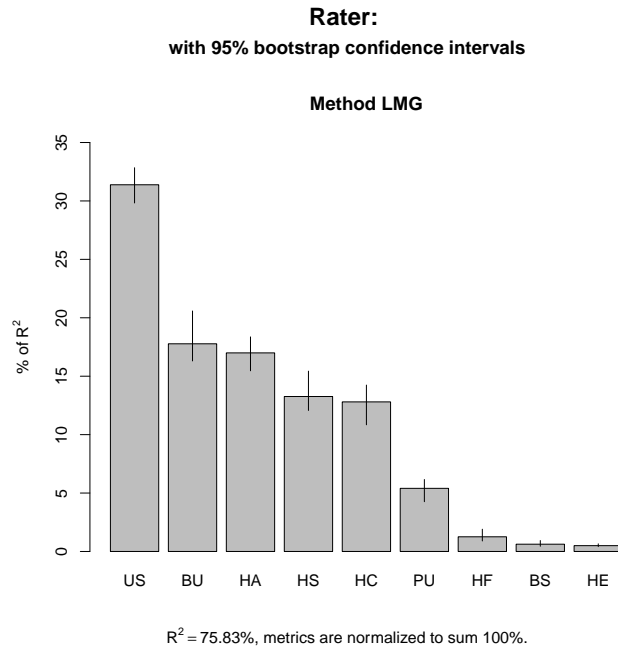
```
out <- raterimp(rv, OQ ~ HE+PU+HC+HS+US+HF+BS+BU+HA, atype="lmg", b=10,
  colforraters="Rater", byrater=FALSE)
```

Note: in a real analysis, you will want to change the number of bootstrap replications from “b=10” to at least 1000.

4. To see a plot of relative importances for predicting OQ:

```
plot(out)
```

²Depends on the package [relaimpo](#)



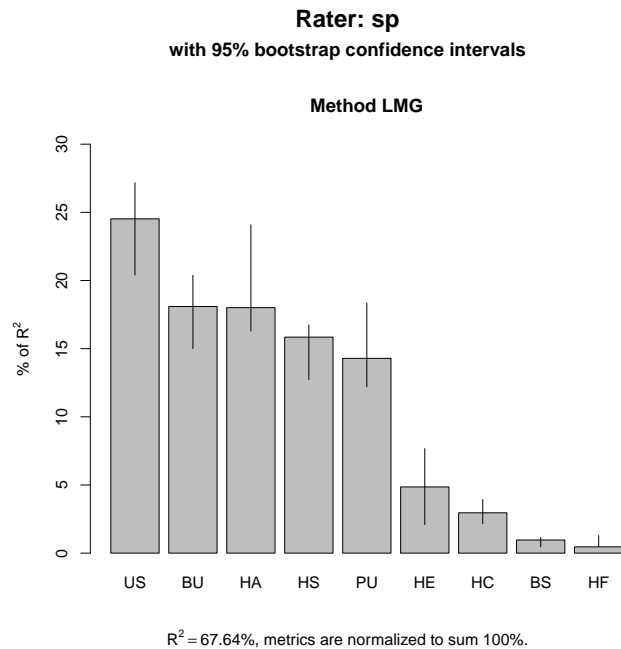
To see a detailed list of many different metrics including confidence intervals:

```
summary(out)
```

- In this study, we were interested in how quality ratings varied across various raters, so we had multiple people rate the same trails. To RI metrics for only the rater Sandra (aka 'sp'), use the following command:

```
out <- raterimp(rv, OQ ~ HE+PU+HC+HS+US+HF+BS+BU+HA, atype="lmg", b=10,
  colforraters="Rater", byrater=TRUE, subset="Year==2")

plot(out, rater="sp")
```



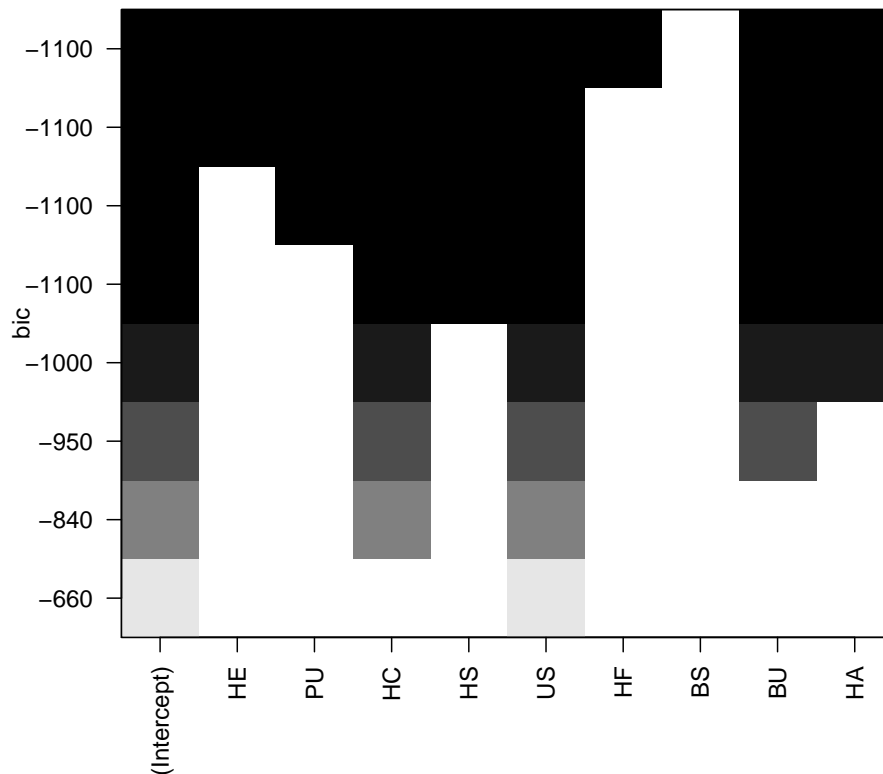
H

Trait Selection

In experimental design of trials designed to breed simultaneously for many horticultural traits, it is often useful to know which traits are more important targets of selection. For example, does variation in trait x explain more variation in overall quality than trait y ? One potentially useful way to assess which traits should be included in your trials is to run the function `ratersub()` which performs an exhaustive search for the best subsets of the traits for predicting OQ using an efficient branch-and-bound algorithm³.

1. To visualize the trait subsetting, run:

```
traitSub <- ratersub(data=rv, formula=OQ ~HE+PU+ HC+ HS+ US +HF+ BS+ BU+ HA,  
  subset="Year==1", b=10, cp="adjr2")  
  
plot(traitSub)
```



H

2. To see a table form of this:

```
table(traitSub)
```

³Depends on the package [leaps](#)

Creating a new trait index

1. `ratervar` can construct new trait indices⁴. To create an average of all traits (excluding “OQ” in this case)

```
traitAverage <- qualityindex(data=rv,traits=c("HE","PU", "HC", "HS", "US","HF",  
      "BS", "BU", "HA"), weights=rep(1/9, 9), normalize=FALSE)
```

2. To create a trait index using coefficients from relative importance analysis⁵:

```
traitRelaImpo <- raterimp(data=rv, formula=OQ~HE+PU+HC+HS+US+HF+BS+BU+HA,  
      colforraters="Rater", byrater=FALSE, b=10)
```

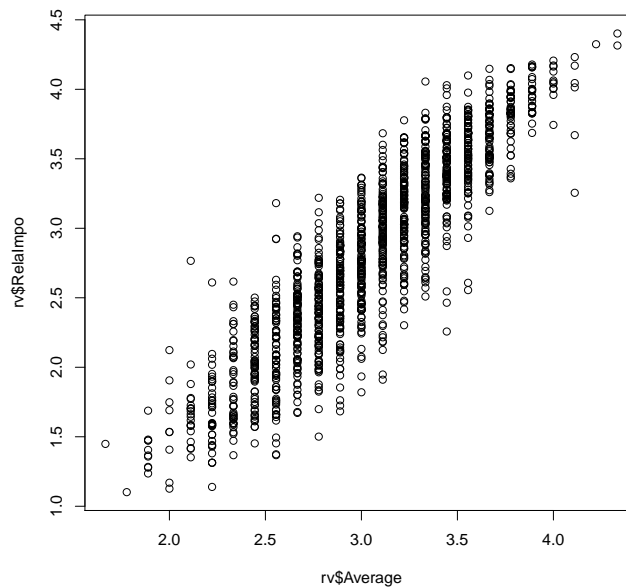
```
traitRelaImpo <- qualityindex(data=rv,traits=c("HE","PU", "HC", "HS", "US","HF",  
      "BS", "BU", "HA"), weights=traitRelaImpo, normalize=FALSE)
```

3. Create new column with indices:

```
rv$Average <-traitAverage  
rv$RelaImpo <-traitRelaImpo
```

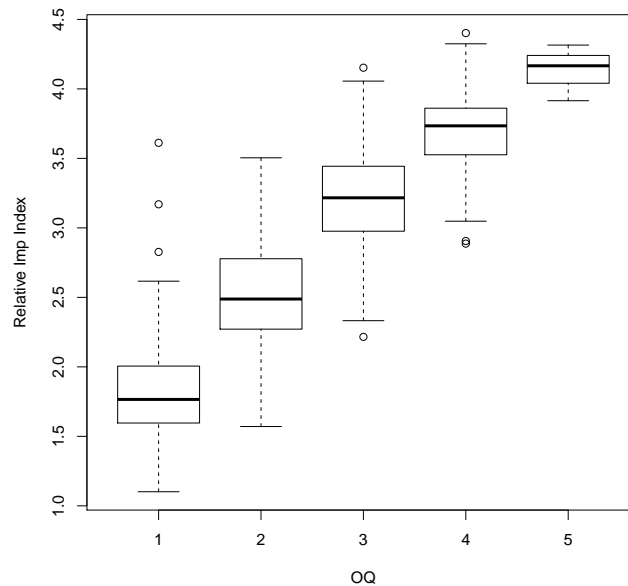
4. Indices can be visually compared in a number of ways, such as:

```
plot(rv$Average, rv$RelaImpo)  
boxplot(rv$RelaImpo~rv$OQ, xlab="OQ", ylab="Rel_Imp_Index")
```



⁴ Or *indexes* for our UK friends.

⁵ Option “byrater=TRUE” will return n columns for n raters.



ICC Values

1. To test the Intra-Class Correlation Coefficients⁶ (ICC) of the **OQ** scores between raters:

```
OQ_RaterICC<-ratericc(data=rv, idcols=1:8, subset=NULL, formula=Planting+Plot
~Rater, qcol="OQ", type="c", model="o")
```

```
OQ_RaterICC
```

Single Score Intraclass Correlation

Model: oneway

Type : consistency

Subjects = 288

Raters = 3

ICC(1) = 0.646

2. To test the ICC between **average score** indices between raters:

```
Ave_RaterICC<-ratericc(data=rv, idcols=1:8, subset=NULL, formula=Planting+Plot
~Rater, qcol="Average", type="c", model="o")
```

```
Ave_RaterICC
```

Single Score Intraclass Correlation

Model: oneway

Type : consistency

Subjects = 288

Raters = 3

ICC(1) = 0.555

The ICC value actually goes down (0.646 to 0.555) when we use an average trait index.

⁶ depends on the package [irr](#)

3. To test the ICC between **relative importance** indices between raters:

```
RI_raterICC<-ratericc(data=rv, idcols=1:8, subset=NULL, formula=Planting+Plot
~Rater, qcol="RelaImpo", type="c", model="o")
```

```
RI_raterICC
```

Single Score Intraclass Correlation

Model: oneway

Type : consistency

Subjects = 288

Raters = 3

ICC(1) = 0.751

4. Does the Relative Importance Index do a statistically better job than OQ scores?⁷

```
RI_raterICC_compare <- ratericc(data=rv, idcols=1:8, subset=NULL, formula=
Planting+Plot~Rater, qcol="RelaImpo", type="c", model="o", r0=0.646)
```

```
RI_raterICC_compare
```

Single Score Intraclass Correlation

Model: oneway

Type : consistency

Subjects = 288

Raters = 3

ICC(1) = 0.751

F-Test, H0: r0 = 0.646 ; H1: r0 > 0.646

F(287,576) = 1.55 , p = 5.23e-06

95%-Confidence Interval for ICC Population Values:

0.707 < ICC < 0.791

Yes, H_0 : ICC=0.646 is rejected, indicating that “Relative Importance” metric does increase consistency between raters.

⁷I included a null hypothesis that the two models are not different by comparing the OQ ICC value as ratervar